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Reviewer: Anne Corrigan

Timestamp: [year=2010; month=5; day=3; hr=16; min=14; sec=47; ms=293;]

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Application No: 10535522 Version No: 4.0

Input Set:

Output Set:

Started: 2010-04-27 12:46:08.469
Finished: 2010-04-27 12:46:09.867
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 398 ms
Total Warnings: 9
Total Errors: 0
No. of SeqIDs Defined: 14
Actual SeqID Count: 14

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SEQUENCE LISTING

<110> Steinkasserer, Alexander

<120> Use of Soluble Forms of CD83 and Nucleic Acids Encoding them for the Treatment or Prevention of Diseases

<130> 032723woJH

<140> 10535522

<141> 2006-04-13

<160> 14

<170> PatentIn version 3.5

<210> 1

<211> 618

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(615)

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gct ccc gcg acg ccg gag gtg aag gtg gct tgc tcc gaa gat gtg gac 96
Ala Pro Ala Thr Pro Glu Val Lys Val Ala Cys Ser Glu Asp Val Asp
20 25 30

ttg ccc tgc acc gcc ccc tgg gat ccg cag gtt ccc tac acg gtc tcc 144
Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser
35 40 45

tgg gtc aag tta ttg gag ggt ggt gaa gag agg atg gag aca ccc cag 192
Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln
50 55 60

gaa gac cac ctc agg gga cag cac tat cat cag aag ggg caa aat ggt 240
Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly
65 70 75 80

tct ttc gac gcc ccc aat gaa agg ccc tat tcc ctg aag atc cga aac 288
Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn
85 90 95

act acc agc tgc aac tcg ggg aca tac agg tgc act ctg cag gac ccg 336
Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro
100 105 110

gat ggg cag aga aac cta agt ggc aag gtg atc ttg aga gtg aca gga 384

Asp Gly Gln Arg Asn Leu Ser Gly Val Ile Leu Arg Val Thr Gly			
115	120	125	
tgc cct gca cag cgt aaa gaa gag act ttt aag aaa tac aga gcg gag			432
Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu			
130	135	140	
att gtc ctg ctg ctg gct ctg gtt att ttc tac tta aca ctc atc att			480
Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile			
145	150	155	160
ttc act tgt aag ttt gca cgg cta cag agt atc ttc cca gat ttt tct			528
Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser			
165	170	175	
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Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys			
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Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser			
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Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln			
50	55	60	
Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly			
65	70	75	80
Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn			
85	90	95	
Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro			
100	105	110	

Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly
115 120 125

Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu
130 135 140

Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile
145 150 155 160

Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser
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His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu Val
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gcc tgc agc ctg gca ccc gcg atg gcg atg cgg gag gtg acg gtg gct 97
Ala Cys Ser Leu Ala Pro Ala Met Ala Met Arg Glu Val Thr Val Ala
15 20 25

tgc tcc gag acc gcc gac ttg cct tgc aca gcg ccc tgg gac ccg cag 145
Cys Ser Glu Thr Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln
30 35 40

ctc tcc tat gca gtg tcc tgg gcc aag gtc tcc gag agt ggc act gag 193
Leu Ser Tyr Ala Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu
45 50 55 60

agt gtg gag ctc ccg gag agc aag caa aac agc tcc ttc gag gcc ccc 241
Ser Val Glu Leu Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro
65 70 75

agg aga agg gcc tat tcc ctg acg atc caa aac act acc atc tgc agc	289
Arg Arg Arg Ala Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser	
80 85 90	
tcg ggc acc tac agg tgt gcc ctg cag gag ctc gga ggg cag cgc aac	337
Ser Gly Thr Tyr Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn	
95 100 105	
ttg agc ggc acc gtg gtt ctg aag gtg aca gga tgc ccc aag gaa gct	385
Leu Ser Gly Thr Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala	
110 115 120	
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Thr Glu Ser Thr Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe	
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Ser Leu Val Val Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe	
145 150 155	
gca cga cta caa agc att ttc cca gat att tct aaa cct ggt acg gaa	529
Ala Arg Leu Gln Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu	
160 165 170	
caa gct ttt ctt cca gtc acc tcc cca agc aaa cat ttg ggg cca gtg	577
Gln Ala Phe Leu Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val	
175 180 185	
acc ctt cct aag aca gaa acg gta tgagtaggat ctccactggc ttttacaaag	631
Thr Leu Pro Lys Thr Glu Thr Val	
190 195	
ccaagggcac atcagatcag tgcgcctgaa tgccacccgg acaagagaag aatgagctcc	691
atcctcagat ggcaaccttt ctttgaagtc cttcacctga cagtggctc cacactactc	751
cctgacacag ggtcttgagc accatcatat gatcacgaag catggagttt caccgcttct	811
ctgtggctgt cagcttaatg tttcatgtgg ctatctggc aacctcgtga gtgctttca	871
gtcatctaca agctatggtg agatgcaggt gaagcagggt catggaaat ttgaacactc	931
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gacaggccaa gctgtgagcc agtggaaat atttagcaaa taatttccca gtgcgaaggt	1111
cctgctatta gtaaggagta ttatgtgtac atagaaatga gaggtcagtg aactattccc	1171
cagcagggcc ttttcatctg gaaaagacat ccacaaaagc agcaatacag agggatgcca	1231
catttatttt ttaatcttc atgtacttgt caaagaagaa ttttcatgt ttttcaaag	1291
aagtgtgttt ctttcctttt ttaaaatatg aaggtctagt tacatagcat tgctagctga	1351
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20 25 30

Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Leu Ser Tyr Ala
35 40 45

Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu Ser Val Glu Leu
50 55 60

Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro Arg Arg Arg Ala
65 70 75 80

Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser Ser Gly Thr Tyr
 85 90 95

Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn Leu Ser Gly Thr
 100 105 110

Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala Thr Glu Ser Thr
115 120 125

Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe Ser Leu Val Val
130 135 140

Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe Ala Arg Leu Gln
145 150 155 160

Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu Gln Ala Phe Leu
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Thr Glu Thr Val
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<220>
<223> Synthetic partial sequence of pGEX2ThCD83ext

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gtg aag gtg gct tgc tcc gaa gat gtg gac ttg ccc tgc acc gcc ccc      96
Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
      10          15           20

tgg gat ccg cag gtt ccc tac acg gtc tcc tgg gtc aag tta ttg gag      144
Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
      25          30           35

ggt ggt gaa gag agg atg gag aca ccc cag gaa gac cac ctc agg gga      192
Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
      40          45           50           55

cag cac tat cat cag aag ggg caa aat ggt tct ttc gac gcc ccc aat      240
Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
      60          65           70

gaa agg ccc tat tcc ctg aag atc cga aac act acc agc tgc aac tcg      288
Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
      75          80           85

ggg aca tac agg tgc act ctg cag gac ccg gat ggg cag aga aac cta      336
Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
      90          95           100

agt ggc aag gtg atc ttg aga gtg aca gga tgc cct gca cag cgt aaa      384
Ser Gly Lys Val Ile Leu Arg Val Thr Gly Cys Pro Ala Gln Arg Lys
      105         110          115

gaa gag act ttt aag aaa tac aga gcg gag att tgagaattca tcgtgact      435
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<220>
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Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
40 45 50 55

Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
60 65 70

Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
75 80 85

Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
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Ser Gly Lys Val Ile Leu Arg Val Thr Gly Cys Pro Ala Gln Arg Lys
105 110 115

Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile
120 125 130

<210> 9
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<212> DNA
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<220>
<223> Synthetic partial sequence of pGEX2ThCD83ext_mut129_CtoS

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Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Gly Thr Pro Glu

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gtg aag gtg gct tgc tcc gaa gat	gtg gac ttg ccc tgc acc gcc ccc		96
Val Lys Val Ala Cys Ser Glu Asp	Val Asp Leu Pro Cys Thr Ala Pro		
10	15	20	
tgg gat ccg cag gtt ccc tac acg gtc tcc tgg gtc aag tta ttg gag			144
Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu			
25	30	35	
ggt ggt gaa gag agg atg gag aca ccc cag gaa gac cac ctc agg gga			192
Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly			
40	45	50	55
cag cac tat cat cag aag ggg caa aat ggt tct ttc gac gcc ccc aat			240
Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn			
60	65	70	
gaa agg ccc tat tcc ctg aag atc cga aac act acc agc tgc aac tcg			288
Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser			
75	80	85	
ggg aca tac agg tgc act ctg cag gac ccg gat ggg cag aga aac cta			336
Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu			
90			